

Delaval, Jan

46767

From: Roark, Jessica  
Sent: Monday, July 16, 2001 7:25 AM  
To: Delaval, Jan  
Subject: 09/484577

Good Morning Jan,

Please search from 09/484577

SEQ ID NO:3.

Please include interference. *ex hly*

Results on paper.

Thanks!

*Jessica H. Roark*

CM1 9B03  
Mailbox 9E12  
Art Unit 1644  
703 605-1209



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2001, 07:35:55 ; Search time 1069.87 seconds

(without alignments)  
7243.256 Million cell updates/sec

Title: US-09-484-577A-3

Perfect score: 501  
Sequence: 1 actccacgacccctccacga.....cagatgcgcgatgatcat 501

Scoring table:

IDENTITY\_XUC  
Gapop 10.0 , Gapext 1.0

Seatched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba1:\*  
2: gb\_ba2:\*  
3: gb\_ba3:\*  
4: gb\_in1:\*  
5: gb\_in2:\*  
6: gb\_in3:\*  
7: gb\_om:\*  
8: gb\_ov:\*  
9: gb\_pat1:\*  
10: gb\_pat2:\*  
11: gb\_ph:\*  
12: gb\_p11:\*  
13: gb\_p12:\*  
14: gb\_p13:\*  
15: gb\_p14:\*  
16: em\_ba1:\*  
17: em\_ba2:\*  
18: em\_fun:\*  
19: em\_htgo\_hum:\*  
20: em\_htgo\_inv:\*  
21: em\_htgo\_rod:\*  
22: em\_htg\_hum1:\*  
23: em\_htg\_hum2:\*  
24: em\_htg\_hum3:\*  
25: em\_htg\_hum4:\*  
26: em\_htg\_hum5:\*  
27: em\_htg\_hum6:\*  
28: em\_htg\_hum7:\*  
29: em\_htg\_hum8:\*  
30: em\_htg\_inv1:\*  
31: em\_htg\_inv2:\*  
32: em\_htg\_ocher:\*  
33: em\_htg\_rod:\*  
34: em\_hum1:\*  
35: em\_hum2:\*  
36: em\_hum3:\*  
37: em\_hum4:\*  
38: em\_hum5:\*  
39: em\_hum6:\*  
40: em\_hum7:\*  
41: em\_in:\*  
42: em\_om:\*  
43: em\_or:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	92.4	18.4	3526	2	AF273216	AF273216 Rhizobium
2	88.8	17.7	28804	3	SSU51197	U51197 Sphingomonas
3	88.8	17.7	28804	9	AR068625	AR068625 sequence
4	85.8	17.3	15552	1	AE004049	AE004049 Xylella f
5	86	17.2	1428	3	NME391263	AJ391263 Neisseria
6	86	17.2	4254	1	AF121772	AF121772 Neisseria
7	86	17.2	7824	3	NME391260	AJ391260 Neisseria
8	86	17.2	11381	1	AE002524	AE002524 Neisseria



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2001, 07:35:55 ; Search time 1171.33 Seconds

(without alignments)  
4043.164 Million cell updates/sec

Title: US-09-484-577A-3

Perfect score: 501

Sequence: 1 actctcagctctcacgca.....cagaatgcygcgatgatcat 501

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*  
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6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*  
12: gb\_est12:\*  
13: gb\_est13:\*  
14: gb\_est14:\*  
15: gb\_est15:\*  
16: gb\_est16:\*  
17: gb\_est17:\*  
18: gb\_est18:\*  
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42: gb\_est42:\*  
43: gb\_est43:\*

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60: em\_esthum26:\*  
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111: em\_esthum77:\*  
112: em\_esthum78:\*  
113: em\_esthum79:\*  
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256: gb\_est187:\*  
257: gb\_est188:\*  
258: gb\_est189:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result					Description				
No.	Score	Query	Match	Length	ID				
C 1	60.6	12.1	932	219	CNS0070E	AL066254	Drosophila	AL066254	Drosophila
C 2	55	11.0	925	219	CNS0091P	AL053013	Drosophila	AL053013	Drosophila
C 3	44.8	8.9	508	31	AV630811	AV630811	AV630811	AV630811	AV630811
C 4	43.6	8.7	772	218	AF075872	AF075872	AF075872	AF075872	AF075872
C 5	42	8.4	839	219	CNS0040B	AL054280	Drosophila	AL054280	Drosophila
C 6	40.8	8.1	932	219	CNS0072C	AL066742	Drosophila	AL066742	Drosophila
C 7	39.8	7.9	639	24	A1770858	A1770858	606059D06	606059D06	606059D06
C 8	39.6	7.9	576	103	AI881920	AI881920	606075806	606075806	606075806
C 9	39.6	7.9	656	1213	CNS01213	AL101589	Drosophila	AL101589	Drosophila
C 10	39.6	7.9	692	219	CNS0070H	AL050923	Drosophila	AL050923	Drosophila
C 11	39.6	7.9	754	110	BF8969678	BF8969678	963014A09	963014A09	963014A09
C 12	39.4	7.9	814	152	BG310235	BG310235	HVSMC001	HVSMC001	HVSMC001
C 13	38.8	7.7	604	164	BE233745	BE233745	HVSMC001	HVSMC001	HVSMC001
C 14	38.8	7.7	604	164	BE233745	BE233745	HVSMC001	HVSMC001	HVSMC001
C 15	38.6	7.7	844	219	CNS0052P	BE215332	HV_CEB000	HV_CEB000	HV_CEB000
C 16	38.4	7.7	925	219	CNS00091P	AL053013	Drosophila	AL053013	Drosophila
C 17	38	7.6	265	151	R01662	R01662	ye76a03_s1	ye76a03_s1	ye76a03_s1
C 18	38	7.6	765	187	BF616985	BF616985	HVSMC001	HVSMC001	HVSMC001
C 19	37.6	7.5	424	167	BEA04013	BEA04013	WHE0410_D	WHE0410_D	WHE0410_D
C 20	37	7.4	392	32	AV644920	AV644920	AV644920	AV644920	AV644920
C 21	37	7.4	393	32	AV644931	AV644931	AV644931	AV644931	AV644931
C 22	37	7.4	424	136	BE497481	BE497481	WHE0753_A	WHE0753_A	WHE0753_A
C 23	37	7.4	539	31	AV640485	AV640485	AV640485	AV640485	AV640485
C 24	37	7.4	667	238	AZ131633	AZ131633	OSNRB011	OSNRB011	OSNRB011
C 25	36.8	7.3	441	137	BE604637	BE604637	WHE1413-1	WHE1413-1	WHE1413-1
C 26	36.8	7.3	510	137	BE858055	BE858055	5-7E-ZO_P	5-7E-ZO_P	5-7E-ZO_P
C 27	36.8	7.3	521	30	AV434008	AV434008	AV434008	AV434008	AV434008
C 28	36.8	7.3	600	31	AV602736	AV602736	AV602736	AV602736	AV602736
C 29	36.8	7.3	649	136	BE490046	BE490046	WHE0364_B	WHE0364_B	WHE0364_B
C 30	36.8	7.3	1101	219	CNS0175Y	AL108046	Drosophila	AL108046	Drosophila
C 31	36.6	7.3	542	152	BG322774	BG322774	EM1_14_A1	EM1_14_A1	EM1_14_A1
C 32	36.6	7.3	543	168	BF705550	BF705550	RH12_4_E	RH12_4_E	RH12_4_E
C 33	36.6	7.3	602	111	AW056288	AW056288	660006F10	660006F10	660006F10
C 34	36.6	7.3	706	137	BE601938	BE601938	HVSMC010	HVSMC010	HVSMC010
C 35	36.6	7.3	734	115	AW348861	AW348861	HV_CEB001	HV_CEB001	HV_CEB001
C 36	36.6	7.3	930	144	BF065890	BF065890	z71C109_1	z71C109_1	z71C109_1
C 37	36.4	7.3	466	162	BE051079	BE051079	z71C109_1	z71C109_1	z71C109_1
C 38	36.4	7.3	547	152	BG314210	BG314210	WHE2460_E	WHE2460_E	WHE2460_E
C 39	36.4	7.3	750	218	AF075552	AF075552	AF075552	AF075552	AF075552
C 40	36.4	7.3	1009	219	CNS010EW	BE404053	Drosophila	BE404053	Drosophila
C 41	36.2	7.2	291	167	BE404053	BE404053	WHE0403_A	WHE0403_A	WHE0403_A
C 42	36.2	7.2	604	167	BE4041916	BE4041916	925009EC4	925009EC4	925009EC4
C 43	36.2	7.2	679	116	AW448165	AW448165	BRY_1330	BRY_1330	BRY_1330
C 44	36.2	7.2	866	152	BG320801	BG320801	Zm04_01e1	Zm04_01e1	Zm04_01e1
C 45	36.2	7.2	1101	219	CNS010QC	AL068542	Drosophila	AL068542	Drosophila

## ALIGNMENTS

RESULT	1
CNS0070E/c	
LOCUS	
DEFINITION	CNS0070E 932 bp DNA GSS 03-JUN-1999
ACCESSION	Drosophila melanogaster genome survey sequence TERN3 end of BAC #
VERSION	BAC1d21 of RPI1-98 library from Drosophila melanogaster (fruit
KEYWORDS	fly), genomic survey sequence.
SOURCE	AL066254
ORGANISM	AL066254.1 GI:4945121
	GSS.
	fruit fly.
	Drosophila
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 932)
AUTHORS	Genoscope.
TITLE	Direct Submission

## JOURNAL

Submitted (02-2-JUN-1999) Genoscope - Centre National de Séquençage  
BP 131 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr  
Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))

Determination of this *Bacillus Drosophila* Genome Project (BDGP) collaboration with the Berkeley *Drosophila* Genome Project (BDGP). The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP *Drosophila melanogaster* BAC library was prepared by Kazutoku Oosawa and Aaron Memmose in Pieret de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

COMMENT

```

source      1. 932
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_id="RPCI-98"
/clone="BACR14D21"
/note="end : TET3"
421 a      135 c      96 g      50 t      230 others
BASE COUNT
ORIGIN

```

Query Match	12.1%	Score 60.6	DB 219	Length 932
Best Local Similarity	29.7%	Pred. No. 5e-06		
Matches 77; Conservative	83;	Mismatches	99;	Indels 0; Gaps 0

[illegible]

## 2

LOCUS	CNS0091P	925 bp	DNA	03-JUN-1999
DEFINITION	Drosophila melanogaster genome survey sequence TENG end of BAC # BACR19D16 of Rpci-98 library from Drosophila melanogaster (fruit fly) genomic survey sequence.			
ACCESSION	AL053013			
VERSION	AL053013.1	GI:4934461		
KEYWORDS	GSS.			
SOURCE	fruit fly.			
ORGANISM	Drosophila melanogaster			
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
	1 (bases 1 to 925)			
REFERENCE	Genoscope.			
AUTHORS	Direct Submission			
TITLE	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage			
JOURNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqet@genoscope.cns.fr			

## COMMENT

- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).  
 The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuo Ogoe and Aaron Mammoser in Pieter de Jong's laboratory at the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

## source

1. 925  
 /organism="Drosophila melanogaster"  
 /db\_xref="taxon:7227"  
 /clone\_lib="RPCL-98"  
 /clone="BACR19D16"  
 /note="end : TET3"

BASE COUNT 120 a 61 c 61 g 172 t 511 others  
 ORIGIN

Query Match 11.0%; Score 55; DB 219; Length 925;  
 Best Local Similarity 14.8%; Pred. No. 0.00016;  
 Matches 57; Conservative 177; Mismatches 145; Indels 6; Gaps 1;

Oy 31 ggcctgtaagtgtgtgctgaggggcaaaacccgagcagctgctctccgcgc 90  
 Db 539 KKGCTTGSTTTTSSGSGTGKCCSSGSGSCSCSCSCSCSCCBBCCCCSS 598  
 Oy 91 cgcctcgaattgctgagcagccatctccacagcagactcacgcgccttct 150  
 Db 599 KCCSSBSSKCSSTSBSCSCCSCSKSVCGTSCSSSSSSSTSSSTSSSKSS 658  
 Oy 151 tgcctctgttctctcgcgcgtgctgagggcagctgagcagcagcagctg 210  
 Db 659 GSSSSSSSSSTTTSTKSTSGSGSWAGGSGSTSTSSSSSSSTSSSVSSG 718  
 Oy 211 tctctcatccagaagatc-----gtgcgggagcagctgtaagctgtgt 264  
 Db 719 TBSGSSBSSSSGSSSTSBBSCTSTSSSSSSSYSTSCCTCCSYSTSSSS 778  
 Oy 265 cgaagtcgagctgtgtgagcagctcagctcagctgagcagcagcagc 324  
 Db 779 TSMGSTGSSSSSVGTSSSDSTSTCCSCCYMCTCCSTYBMCYTSTSCG 838  
 Oy 325 gattctgagcagctgagctcagctgagctgagctgagctgagctgag 384  
 Db 839 GVTKCGCGCGSSSTNGMBGTSSACSSSSSSSVSSSSKSMASSSSVSS 898  
 Oy 385 catcaaggtgtcgcgcgccacaga 409  
 Db 899 NSSSASKSSSSGVSAGSGSGSV 923

RESULT 3  
 AV630811/c 508 bp mRNA EST 15-DEC-2000  
 LOCUS AV630811 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas  
 DEFINITION reinhardtii cDNA clone LC1084f07\_5', mRNA sequence.  
 ACCESSION AV630811  
 VERSION AV630811.1 GI:10793445  
 KEYWORDS EST.  
 SOURCE Chlamydomonas reinhardtii.  
 ORGANISM Chlamydomonas reinhardtii.  
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 Chlamydomonadales; Chlamydomonas.  
 REFERENCE 1 (bases 1 to 508)  
 Location/Qualifiers

## AUTHORS

Asamizu, E., Miura, K., Kuchio, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,  
 Nakamura, Y., and Tabata, S.  
 Generation of expressed sequence tags from low-CO2 and high-CO2  
 adapted cells of Chlamydomonas reinhardtii  
 DNA Res. 7 (5), 305-307 (2000)

## JOURNAL

## MEDLINE

20539644

## COMMENT

Contact: Erika Asamizu  
 The First Laboratory for Plant Gene Research  
 Kazusa DNA Research Institute  
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
 Email: [asamizu@kazusa.or.jp](mailto:asamizu@kazusa.or.jp), URL: <http://www.kazusa.or.jp/en/plant/>.

## FEATURES

## source

1. 508  
 /organism="Chlamydomonas reinhardtii"  
 /strain="C9"  
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 /clone\_lib="LC1084f07\_5"  
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BASE COUNT 69 a 194 c 172 g 72 t 1 others  
 ORIGIN

Query Match 8.9%; Score 44.8; DB 31; Length 508;  
 Best Local Similarity 52.1%; Pred. No. 0.08;  
 Matches 100; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

Oy 5 tccacccctccacccagagatgaagtcgctcgtgtagtgtgtcgtcggggcaaac 64  
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 Oy 65 cggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 124  
 Db 271 AGCGCGGAGGCGACCGACGAGTGGCGAGTGGCGAGGACGACATGATGCA 212  
 Oy 125 accggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 184  
 Db 211 TGCGCGCCCATGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 152  
 Oy 185 ggtctcgcagag 196  
 Db 151 GTGATGCGCATG 140

RESULT 4  
 AF075872/c 772 bp DNA GSS 29-AUG-2000  
 LOCUS AF075872 Salmonella typhimurium LT2, Lambda DMSH II Salmonella  
 DEFINITION typhimurium genomic clone 142-T3, DNA sequence.  
 ACCESSION AF075872  
 VERSION AF075872.1 GI:3320742  
 KEYWORDS GSS.  
 SOURCE Salmonella typhimurium.  
 ORGANISM Salmonella typhimurium.  
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 Salmonella.

## REFERENCE

1 (bases 1 to 772)

Wong, R.M.-Y., Wong, K.K., Benson, N.R., and McClelland, M.  
 Sample sequencing of a Salmonella typhimurium LT2 lambda library:  
 comparison to the Escherichia coli K12 genome

FEMS Microbiol. Lett. 173 (2), 411-423 (1999)

## JOURNAL

## MEDLINE

99243757

## COMMENT

Contact: McClelland, M  
 Molecular Biology  
 Sidney Kimmel Cancer Center  
 3099 Science Park Road, San Diego, CA 92121, USA  
 Email: [mcclelland@lifsci.sdsu.edu](mailto:mcclelland@lifsci.sdsu.edu)  
 Class: shotgun.  
 Location/Qualifiers

## FEATURES



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2001, 07:36:00 ; Search time 126.18 Seconds  
(without alignments)  
2493.095 Million cell updates/sec

Title: US-09-484-577A-3  
Perfect score: 501  
Sequence: 1 actctccagcctctaccga.....cagaatgcgcgatcatcat 501

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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22: /SIDSI/gcgdata/geneseq/geneseq/NA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	88.8	17.7	28804	17	AAT37329
C 2	88.8	17.7	28804	18	AAT92474
C 3	88.8	17.7	28804	20	AAV99812
C 4	88.8	17.7	28804	20	AAV81474
C 5	86	17.2	1305	21	AAZ54336
C 6	86	17.2	1428	21	AAZ54335
C 7	86	17.2	24158	21	AAAB1532
C 8	86	17.2	34980	21	AAAF21611
C 9	86	17.2	34980	21	AAAF21612
C 10	86	17.2	837096	21	AAA81489
C 11	51.6	10.3	5120	18	AAT73218

12	51.6	10.3	5120	21	AAZ88585
13	47.8	9.5	6400	20	AAZ22701
14	45	9.0	7184	15	AAO70050
15	43.4	8.7	7183	11	AAO60704
16	43	8.6	24379	18	AAV93095
17	43	8.6	24379	19	AAV25925
C 18	39	7.8	1998	22	AAV72013
C 19	37.6	7.5	10732	21	AAAI0594
C 20	37.2	7.4	1194	17	AAT58555
C 21	37.2	7.4	4496	17	AAT58553
C 22	37.2	7.4	58857	21	AAV58471
C 23	37	7.4	1951	19	AAV11459
C 24	37	7.4	1981	21	AAZ50482
C 25	36.2	7.2	16020	21	AAV39283
C 26	36	7.2	1136	21	AAV47742
C 27	35.8	7.1	836	19	AAV62157
C 28	35.8	7.1	3765	21	AAV55782
C 29	35.8	7.1	53500	21	AAV55842
C 30	35.8	7.1	117213	19	AAV62176
C 31	35.4	7.0	48300	22	AAV61281
C 32	35	7.0	2025	21	AAV49036
C 33	34.8	6.9	1470	21	AAV38391
C 34	34.8	6.9	11279	21	AAV38389
C 35	34.6	6.9	8438	15	AAV38389
C 36	34.4	6.9	1830	22	AAV38389
C 37	34.4	6.9	10095	19	AAV38389
C 38	34.2	6.8	10095	19	AAV38389
C 39	34	6.8	1758	13	AAV31765
C 40	34	6.8	1758	13	AAV31765
C 41	34	6.8	2061	10	AAV290321
C 42	34	6.8	3632	17	AAV06978
C 43	34	6.8	3632	19	AAV21373
C 44	34	6.8	49272	20	AAV35000
C 45	34	6.8	114955	20	AAV35491

#### ALIGNMENTS

RESULT 1	
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ID	AAT37329 standard; DNA: 28804 BP.
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AC	AAT37329;
XX	
DF	30-NOV-1996 (first entry)
XX	
DE	Sphingian biosynthetic gene region.
XX	
KW	Sphingian; polysaccharide; spsB gene; glucosyl-IP-transferase; ds.
XX	
OS	Sphingomonas strain S88 (ATCC 31554).
XX	
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FT	complement (3311..3313)
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FT	complement (5323..5325)
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FT	/note= "spsR gene putative initiation codon"
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FT	
FT	CDS

A. pleuropneumonia  
Pseudomonas fluores  
px gene of Pasteu  
Sequence encoding  
Streptomyces fireo  
Streptomyces roseo  
Corynebacterium q1  
Gene encoding a su  
Streptomyces prist  
Streptomyces prist  
Nucleotide sequenc  
C. acidivorans gam  
Corn sulphate perm  
Streptomyces nogal  
Zea mays DNA fragm  
Nucleotide sequenc  
Complete nucleotid  
HSV-2 strain SB5 C  
N. magdali bacter  
DNA encoding a hig  
Pseudomonas sp. WF  
Pseudomonas sp. WF  
DNA encoding pseud  
Wheat Nph2-2 prote  
Mycobacterium tube  
CDNA clone p7f enc  
Rat hepatocyte nuc  
Sequence encoding  
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Thermus thermophil  
Mycobacteriophage  
Human adenosine A1

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FT	CDS	15883..15885
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XX		
PF	24-JAN-1996;	96EP-0300467.
XX		
XX	24-JAN-1995;	95US-0377440

XX (SHIN-) SHINETSU BIO INC.  
PA (SHIE ) SHINETSU CHEM CO LTD.  
PI Armentrout RM, Mikolajczak M, Pollock TJ, Thorne L,  
PI Yamazaki M;  
DR WPI: 1996-386292/39.  
DR P-P.SDB: AAM03997.  
XX  
XX New isolated DNA from *Sphingomonas* sp. - used for transforming  
PT recipient bacteria to obtain hyper-producers of sphingan  
PT polysaccharide(s).  
XX  
PS Claim 32; Page 56-70; 105pp; English.

A 28.8 kb chromosomal fragment of *Sphingomonas* strain S88 was isolated on the basis of its ability to restore sphingan biosynthetic capability to *Sphingomonas* mutant S88m260. It contains 23-25 genes, including *sps* genes coding for biosynthesis of the polysaccharide sphingan, *rhs* genes coding for dTMP-(L)rihamnose biosynthesis, *atrD*B genes coding for a transport function and some unidentified open translation reading frames (*urf*). The *spsB* gene was identified that is believed to code for glucosyl IP-transferase (AAM03997), an enzyme catalysing the first step of assembly of sphingan carbohydrates. DNA fragments of S88 can be inserted into a vector in multiple copies and used to produce engineered bacteria that are hyper-producers of sphingan.

Sequence 28804 BP; 4974 A; 9806 C; 9228 G; 4796 T; 0 other;

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	Matches 165;	Conservative	0;	Mismatches 127;	Indels	0; Gaps
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Db	18808	TTCCTGCGGGCGCGCCTCGAGATCATCGAATCCGCCTGCCGTGCCACCCCGCGCTCAACC	18749			
Oy	140	gcgcgccttgcttgcgtgccttgtttctactcghgcgcgcyggcggttcggcgagtc	199			
Db	18748	GCCCGGGTATGTTGGTGCGGGGCTGGCGATCACACCGCTGCTGGCAATCGGCCGCTG	18689			
Oy	200	gacatcgtttgctctgcacccagaagaatcgtgcgcggcgagaccgtgttaagcttgltcag	259			
Db	18688	GAAATGCTGGCCCCGACGACGAGGGCGCGCATCGCCCGATCGCGGAGAACCAAGATCTGCAG,	18629			
Oy	260	cgcctcgaagtgcgcgttggtgcggccactcatctgcgtagtgcgataaggccaacgcgtcaagc	319			
Db	18628	TCCCCCGAAGAAGCGGATCTCTCCGGCCATTCTGTGGGAGAGGGGCGAAGATTCGAAG	18569			
Oy	320	ggcgcgatcttatcgaagctgatgataccatccgcggcggtgtgtagtcttcgcg	371			
Db	18568	GCGCAGTCTGATCAGCTTCATCCACCACATGTGGCAGCCGAAAGCCCGCGC	18517			
RESULT	2					
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ID	AAT92474	standard; DNA; 28804 BP.				
AC	AAT92474;					
DT	04-FEB-1998	(first entry)				
DE	Sphingomonas genus microbe isolated DNA sequence producing sphingan.					
KX	Sphingomonas microbe; sphingan polysaccharide biosynthesis gene;					
KW	sphingan S-88; spsB gene; ss.					
OS	Sphingomonas sp.					
PN	JF09252775-A.					

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2001, 07:36:00 ; Search time 62.76 seconds  
(without alignments)  
1478.895 Million cell updates/sec

Title: US-09-484-577a-3

Perfect score: 501  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Sequences: 317530 seqs, 92630169 residues

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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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6: /cgn2\_6/ptodata/2/ina/Backfillseq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	88.8	17.7	28804	2	US-08-592-874-1	Sequence 1, Appli
2	88.8	17.7	28804	3	US-09-096-942-2	Sequence 2, Appli
3	88.8	17.7	28804	3	US-09-096-867-2	Sequence 2, Appli
4	51.6	10.3	5120	3	US-08-772-270A-6	Sequence 6, Appli
5	51.6	10.3	8370	2	US-08-488-706-1	Sequence 1, Appli
6	37	7.4	1951	3	US-08-922-865-1	Sequence 1, Appli
7	34.6	6.9	8438	1	US-07-945-283-1	Sequence 1, Appli
8	34.4	6.9	1879	2	US-08-403-852D-5	Sequence 3, Appli
9	34.4	6.9	1879	3	US-08-510-646B-5	Sequence 5, Appli
10	34.4	6.9	1879	4	US-09-231-818-5	Sequence 5, Appli
11	34.2	6.8	10095	3	US-08-822-586-45	Sequence 45, Appli
12	34.2	6.8	1758	1	US-08-078-222B-1	Sequence 1, Appli
13	34	6.8	1758	2	US-08-661-330A-1	Sequence 1, Appli
14	34	6.8	1758	3	US-09-038-217A-1	Sequence 1, Appli
15	34	6.8	43272	1	US-08-614-770A-1	Sequence 1, Appli
16	33.2	6.6	2293	1	US-08-604-913B-12	Sequence 12, Appli
17	33.2	6.6	3004	1	US-08-276-213-6	Sequence 6, Appli
18	33.2	6.6	5970	4	US-09-320-878-21	Sequence 21, Appli
19	33.2	6.6	5247	1	US-08-920-812-15	Sequence 15, Appli
20	32.8	6.5	5247	1	US-08-920-827-15	Sequence 15, Appli
21	32.8	6.5	5247	1	US-08-921-177-15	Sequence 15, Appli
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24	32.4	6.5	3877	2	US-08-599-895-1	Sequence 1, Appli
25	32.4	6.5	3877	3	US-09-211-290-1	Sequence 1, Appli
26	32.4	6.5	3877	4	US-09-322-676-1	Sequence 1, Appli
27	32.2	6.4	720	4	US-08-998-416-662	Sequence 662, App

28	32.2	6.4	783	1	US-08-264-861A-11	Sequence 11, Appli
29	32.2	6.4	783	5	PCT-US95-07784-11	Sequence 11, Appli
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33	31.8	6.3	3292	4	US-09-320-878-22	Sequence 22, Appli
34	31.8	6.3	4465	2	US-08-620-605D-1	Sequence 1, Appli
35	31.8	6.3	4547	2	US-09-005-232A-1	Sequence 1, Appli
36	31.8	6.3	11907	4	US-08-061-376-4	Sequence 4, Appli
37	31.8	6.3	20235	1	US-07-642-734C-3	Sequence 3, Appli
38	31.8	6.3	20235	3	US-08-439-009A-3	Sequence 3, Appli
39	31.8	6.3	38506	4	US-09-320-878-19	Sequence 19, Appli
40	31.6	6.3	80161	4	US-09-036-987A-1	Sequence 1, Appli
41	31.4	6.3	1151	1	US-07-704-288C-2	Sequence 2, Appli
42	31.4	6.3	1151	1	US-08-093-372-1	Sequence 1, Appli
43	31.4	6.3	1151	1	US-08-379-259-2	Sequence 2, Appli
44	31.4	6.3	1668	4	US-09-385-028-20	Sequence 20, Appli
45	31.4	6.3	2936	2	US-08-714-677-10	Sequence 10, Appli

#### ALIGNMENTS

RESULT 1  
US-08-592-874-1/c  
; Sequence 1, Application US/08592874  
; Patent No. 5854034  
; GENERAL INFORMATION:  
; APPLICANT: POLLOCK, THOMAS J.  
; APPLICANT: YAMAZAKI, MOTOHIDE  
; APPLICANT: THORNE, LINDA  
; APPLICANT: MIKOLAJCZAK, MARCIA  
; APPLICANT: ARMENTROUT, RICHARD W.  
; TITLE OF INVENTION: DNA SEGMENTS AND METHODS FOR INCREASING  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: JULES E. GOLDBERG  
; STREET: 261 MADISON AVENUE  
; CITY: NEW YORK  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10016-2391  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/592,874  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/377,440  
; FILING DATE: 24-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GOLDBERG, JULES E.  
; REGISTRATION NUMBER: 24,408  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-986-4090  
; TELEFAX: 212-818-9479  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28804 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; FRAGMENT TYPE: N-terminal  
; US-08-592-874-1

Query Match 17.7%; Score 88.8; DB 2; Length 28804;

